

WEST

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 JPO Abstracts Database
 EPO Abstracts Database
 Derwent World Patents Index

Database: IBM Technical Disclosure Bulletins

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L6

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DATE: Friday, February 14, 2003 [Printable Copy](#) [Create Case](#)

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DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ

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<u>L5</u>	L3 same (cDNA or clone)	52	<u>L5</u>
<u>L4</u>	L3 same (uncoupling or splicing or carrier)	36	<u>L4</u>
<u>L3</u>	(mitochondri\$ adj protein)	480	<u>L3</u>
<u>L2</u>	uncoupling protein	233	<u>L2</u>
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WEST

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L1: Entry 1 of 1

File: USPT

Jul 30, 2002

DOCUMENT-IDENTIFIER: US 6426362 B1

TITLE: Formulations of tocopherols and methods of making and using them

Other Reference Publication (35):

Kowaltowski, Alicia J. et al. (1998). "Activation of the potato plant uncoupling mitochondrial protein inhibits reactive oxygen species generation by the respiratory chain" FEBS Letters 425:213-216.

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Search Results - Record(s) 1 through 8 of 8 returned.☐ 1. Document ID: US 20020110808 A1

L6: Entry 1 of 8

File: PGPB

Aug 15, 2002

PGPUB-DOCUMENT-NUMBER: 20020110808

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020110808 A1

TITLE: Toxicant-induced differential gene expression

PUBLICATION-DATE: August 15, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Reidhaar-Olson, John F.	Montclair	NJ	US	

US-CL-CURRENT: 435/6; 435/91.2, 536/23.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWC	Draw Desc	Image
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☐ 2. Document ID: US 20020059663 A1

L6: Entry 2 of 8

File: PGPB

May 16, 2002

PGPUB-DOCUMENT-NUMBER: 20020059663

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020059663 A1

TITLE: Expressed sequences of arabidopsis thaliana

PUBLICATION-DATE: May 16, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Gorlach, Jorn	Durham	NC	US	
An, Yong-Qiang	San Diego	CA	US	
Hamilton, Carol M.	Apex	NC	US	
Price, Jennifer L.	Raleigh	NC	US	
Raines, Tracy M.	Durham	NC	US	
Yu, Yang	Matinsville	NJ	US	
Rameaka, Joshua G.	Durham	NC	US	
Page, Amy	Durham	NC	US	
Mathew, Abraham V.	Cary	NC	US	
Ledford, Brooke L.	Holly Springs	NC	US	
Woessner, Jeffrey P.	Hillsborough	NC	US	
Haas, William David	Durham	NC	US	
Garcia, Carlos A.	Carrboro	NC	US	
Kricker, Maja	Pittsboro	NC	US	
Slater, Ted	Apex	NC	US	
Davis, Keith R.	Durham	NC	US	
Allen, Keith	Cary	NC	US	
Hoffman, Neil	Chapel Hill	NC	US	
Hurban, Patrick	Raleigh	NC	US	

US-CL-CURRENT: 800/298; 435/320.1, 435/419, 530/350, 536/23.6

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw Desc	Image
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☐ 3. Document ID: US 20020048759 A1

L6: Entry 3 of 8

File: PGPB

Apr 25, 2002

PGPUB-DOCUMENT-NUMBER: 20020048759

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020048759 A1

TITLE: Compositions and methods for the therapy and diagnosis of ovarian and endometrial cancer

PUBLICATION-DATE: April 25, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Xu, Jiangchun	Bellevue	WA	US	
Pyle, Ruth A.	Seattle	WA	US	
Stolk, John A.	Bothell	WA	US	

US-CL-CURRENT: 435/6; 424/155.1, 424/93.21, 435/325, 435/69.1, 435/7.23, 514/12, 514/44, 536/23.5

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw Desc	Image
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☐ 4. Document ID: US 20010051335 A1

L6: Entry 4 of 8

File: PGPB

Dec 13, 2001

PGPUB-DOCUMENT-NUMBER: 20010051335

PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20010051335 A1

TITLE: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

PUBLICATION-DATE: December 13, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
LALGUDI, RAGHUNATH V.	CLAYTON	MO	US	
ITO, LAURA Y.	PLEASANTON	CA	US	
SHERMAN, BRADLEY K.	OAKLAND	CA	US	

US-CL-CURRENT: 435/6; 435/69.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KWIC	Draw Desc	Image
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☐ 5. Document ID: US 6500670 B1

L6: Entry 5 of 8

File: USPT

Dec 31, 2002

US-PAT-NO: 6500670
DOCUMENT-IDENTIFIER: US 6500670 B1

TITLE: Plant pyruvate dehydrogenase kinase gene

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KWIC	Draw Desc	Image
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☐ 6. Document ID: US 6476212 B1

L6: Entry 6 of 8

File: USPT

Nov 5, 2002

US-PAT-NO: 6476212
DOCUMENT-IDENTIFIER: US 6476212 B1

TITLE: Polynucleotides and polypeptides derived from corn ear

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KWIC	Draw Desc	Image
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☐ 7. Document ID: US 6335170 B1

L6: Entry 7 of 8

File: USPT

Jan 1, 2002

US-PAT-NO: 6335170
DOCUMENT-IDENTIFIER: US 6335170 B1

TITLE: Gene expression in bladder tumors

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KWIC	Draw Desc	Image
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☐ 8. Document ID: US 6239264 B1

L6: Entry 8 of 8

File: USPT

May 29, 2001

US-PAT-NO: 6239264

DOCUMENT-IDENTIFIER: US 6239264 B1

TITLE: Genomic DNA sequences of ashbya gossypii and uses thereof

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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MMC	Draw Desc	Image
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Terms	Documents
L4 same (cDNA or clone)	8

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SEA MITOCHONDRIAL PROTEINS

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L1 QUE MITOCHONDRIAL PROTEINS

FILE 'CAPLUS, BIOSIS, MEDLINE, SCISEARCH, EMBASE, BIOTECHNO, TOXCENTER, ESBIOBASE, LIFESCI' ENTERED AT 07:49:30 ON 14 FEB 2003

L2 21 S L1 AND (SOLUTE CARRIER OR RNA SPLIC?)

L3 14 DUP REM L2 (7 DUPLICATES REMOVED)

L4 2 S L3 AND (CDNA OR CLONE)

=> d l3 ibib ab 1-14

L3 ANSWER 1 OF 14 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2000:235499 CAPLUS

DOCUMENT NUMBER: 133:172669

TITLE: Computational identification of cis-acting elements affecting post-transcriptional control of gene expression in *Saccharomyces cerevisiae*

AUTHOR(S): Anderson, John S. Jacobs; Parker, Roy

CORPORATE SOURCE: Department of Molecular and Cellular Biology, University of Arizona, Tucson, AZ, 85721, USA

SOURCE: Nucleic Acids Research (2000), 28(7), 1604-1617

CODEN: NARHAD; ISSN: 0305-1048

PUBLISHER: Oxford University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Understanding the regulation of gene expression requires the identification of cis-acting control elements that modulate gene function. The recent availability of complete genome sequences and profiles of mRNA expression has facilitated the development and utilization of computational methods to identify discrete regulatory elements. We have developed an oligomer counting method that identifies sequences that occur significantly more often in a group of interest relative to other genes in the genome. The use of a second parameter, which measures the frequency of oligomers within the group of interest, allows the detection of false pos. signals caused by very infrequent oligomers that would otherwise appear as significant. Applying this method to gene groups that have a common expression pattern or shared function should identify oligomers that comprise cis-acting control elements. As a test of this method, we applied this approach to a set of intron-contg. yeast genes, where we easily identified the known splicing signals as control elements. We have used this training set to examine how this method is affected by the length of the oligomer examd., as well as the size and compn. of the gene group. These simulations allowed us to identify rules for selecting groups of genes to analyze. Finally, application of this method to nuclear genes encoding proteins targeted to the mitochondria identified a new putative cis-acting sequence in the 3'-untranslated region of this family of genes, which may play a role in mRNA localization or the regulation of mRNA stability or translation.

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 2 OF 14 MEDLINE

ACCESSION NUMBER: 2000395377 MEDLINE

DOCUMENT NUMBER: 20374967 PubMed ID: 10913632

TITLE: Splicing before import - an intein in a mitochondrially targeted preprotein folds and is catalytically active in the cytoplasm in vivo.

AUTHOR: Williams L R; Ellis S R; Hopper A K; Davis E O; Martin N C

CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, University of Louisville School of Medicine, KY 40202, USA.

SOURCE: FEBS LETTERS, (2000 Jul 7) 476 (3) 301-5.

Journal code: 0155157. ISSN: 0014-5793.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200008

ENTRY DATE: Entered STN: 20000824

Last Updated on STN: 20000824

Entered Medline: 20000816

AB Nuclear-encoded mitochondrial proteins are

cytoplasmically synthesized and imported into the organelle. The intein-containing RecA protein of *Mycobacterium tuberculosis*, with or without the CoxIVp mitochondrial targeting signal (MTS), was used to determine where a protein targeted to mitochondria folds and becomes catalytically active. Analysis of fractions from *Saccharomyces cerevisiae* cells expressing RecA without the MTS revealed that RecA and intein proteins remained cytoplasmic. With the MTS, most of RecA was directed to mitochondria, while most of the intein remained in the cytoplasm. The intein therefore folds into a catalytically active state in the cytoplasm prior to RecA import into mitochondria.

L3 ANSWER 3 OF 14 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1
 ACCESSION NUMBER: 2000:242695 CAPLUS
 DOCUMENT NUMBER: 133:189409
 TITLE: Defective splicing of the first nad4 intron is associated with lack of several complex I subunits in the *Nicotiana sylvestris* NMS1 nuclear mutant
 AUTHOR(S): Brangeon, Judy; Sabar, Mohammed; Gutierrez, Sophie; Combettes, Bruno; Bove, Jerome; Gendy, Cyrille; Chetrit, Philippe; Colas des Francs-Small, Catherine; Pla, Magali; Vedel, Fernand; De Paepe, Rosine
 CORPORATE SOURCE: Institut de Biotechnologie des Plantes, UMR 8618-CNRS, Universite Paris-Sud, Orsay, 91405, Fr.
 SOURCE: Plant Journal (2000), 21(3), 269-280
 CODEN: PLJUED; ISSN: 0960-7412
 PUBLISHER: Blackwell Science Ltd.
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB In this work, the authors provide evidence for the existence of a nuclear factor involved in the splicing of a specific mitochondrial intron in higher plants. In the *Nicotiana sylvestris* nuclear NMS 1 mutant, defective in both vegetative and reproductive development, the first intron of the nad4 transcript encoding the complex I NAD4 subunit is not removed, whatever the tissue analyzed. Transcript patterns of other std. mitochondrial genes are not affected in NMS1. However, numerous polypeptides are missing in two-dimensional in organello mitochondrial protein synthesis patterns and several nuclear and mitochondrial complex I subunits are present in trace amts. This indicates that translational or post-translational steps in the synthesis of other **mitochondrial proteins** are affected. All of these defects cosegregated with the abnormal phenotype in the offspring of a NMS1 .times. wild-type cross, showing that they are controlled by the same nuclear gene (MS1) or tightly linked loci. Such a complex situation has been described in chloroplasts and mitochondria of fungi, but never in higher plant mitochondria.
 REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 4 OF 14 CAPLUS COPYRIGHT 2003 ACS
 ACCESSION NUMBER: 1999:555234 CAPLUS
 DOCUMENT NUMBER: 132:59810
 TITLE: Transfer of rps14 from the mitochondrion to the nucleus in maize implied integration within a gene encoding the iron-sulphur subunit of succinate dehydrogenase and expression by alternative splicing
 AUTHOR(S): Figueroa, Pablo; Gomez, Isabel; Holuigue, Loreto; Araya, Alejandro; Jordana, Xavier
 CORPORATE SOURCE: Departamento de Genetica Molecular y Microbiologia, Facultad de Ciencias Biologicas, P. Universidad Catolica de Chile, Santiago, 114-D, Chile
 SOURCE: Plant Journal (1999), 18(6), 601-609
 CODEN: PLJUED; ISSN: 0960-7412
 PUBLISHER: Blackwell Science Ltd.
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB The maize mitochondrial genome does not contain a gene coding for ribosomal protein S14. In this paper the authors show that the functional rps14 gene was translocated to the nucleus and acquired the signals conferring expression and product targeting to the mitochondrion in a way not previously described. Transferred rps14 was found integrated between both exons of a gene encoding the iron-sulfur subunit of the respiratory complex II (sdh2). Sdh2 exon 1 and rps14 were sep'd. by a typical plant nuclear intron that was spliced to give a mature poly(A)+ mRNA of 1.4 kb. This processed mRNA encoded a chimeric SDH2 (truncated)-RPS14 polypeptide, and the authors show that this chimeric polypeptide is targeted into isolated plant mitochondria, where it is proteolytically processed in a complex way. An alternative splicing event utilizing the same 5' splice site and a different downstream 3' splice site generated a second mature poly(A)+ mRNA of 1.3 kb that contained both sdh2 exons. This sdh2 transcript encoded an SDH2 polypeptide highly conserved compared with its homologues in other organisms, and it contained the three cysteine-rich clusters that made up the three nonheme iron-sulfur centers responsible for electron transport. To our knowledge, these results constitute the first evidence of alternative splicing playing a role in the expression and targeting of two **mitochondrial proteins** with different functions from the same gene.

REFERENCE COUNT: 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 5 OF 14 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.DUPLICATE 2
ACCESSION NUMBER: 1999195241 EMBASE
TITLE: Mitochondrial assembly in yeast.
AUTHOR: Grivell L.A.; Artal-Sanz M.; Hakkaart G.; De Jong L.; Nijtmans L.G.J.; Van Oosterum K.; Siep M.; Van der Spek H.
CORPORATE SOURCE: L.A. Grivell, Section for Molecular Biology, Institute Molecular Cell Biology, University of Amsterdam, Kruislaan 318, 1098 SM Amsterdam, Netherlands
SOURCE: FEBS Letters, (1999) 452/1-2 (57-60).
Refs: 40
ISSN: 0014-5793 CODEN: FEBLAL
PUBLISHER IDENT.: S 0014-5793(99)00532-3
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 029 Clinical Biochemistry
004 Microbiology
037 Drug Literature Index
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The yeast *Saccharomyces cerevisiae* is likely to be the first organism for which a complete inventory of **mitochondrial proteins** and their functions can be drawn up. A survey of the 340 or so proteins currently known to be localised in yeast mitochondria reveals the considerable investment required to maintain the organelle's own genetic system, which itself contributes seven key components of the electron transport chain. Translation and respiratory complex assembly are particularly expensive processes, together requiring around 150 of the proteins so far known. Recent developments in both areas are reviewed and approaches to the identification of novel **mitochondrial proteins** are discussed. Copyright (C) 1999 Federation of European Biochemical Societies.

L3 ANSWER 6 OF 14 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.DUPLICATE 3
ACCESSION NUMBER: 95271695 EMBASE
DOCUMENT NUMBER: 1995271695
TITLE: Cloning of glutaryl-CoA dehydrogenase cDNA, and expression of wild type and mutant enzymes in *Escherichia coli*.
AUTHOR: Goodman S.I.; Kratz L.E.; DiGiulio K.A.; Biery B.J.; Goodman K.E.; Isaya G.; Frerman F.
CORPORATE SOURCE: Department of Pediatrics, University Colorado School

SOURCE: Medicine, Denver, CO, United States
Human Molecular Genetics, (1995) 4/9 (1493-1498).
ISSN: 0964-6906 CODEN: HMGEE5
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry

LANGUAGE: English

SUMMARY LANGUAGE: English

AB We have cloned, sequenced, and expressed cDNAs encoding wild type human glutaryl-CoA dehydrogenase subunit, and have expressed a mutant enzyme found in a patient with glutaric acidemia type I. The mutant protein is expressed at the same level as the wild type in *Escherichia coli*, but has less than 1% of the activity of wild-type dehydrogenase. We also present evidence that the glutaryl-CoA dehydrogenase transcript is alternatively spliced in human fibroblasts and liver; the alternatively spliced mRNA, when expressed in *E. coli*, encodes a stable but inactive protein. Purified expressed human glutaryl-CoA dehydrogenase has kinetic constants similar to those of the previously purified porcine dehydrogenase. The primary translation product from in vitro transcribed glutaryl-CoA dehydrogenase mRNA is translocated into mitochondria and processed in the same manner as most other nuclear-encoded **mitochondrial proteins**. Human glutaryl-CoA dehydrogenase shows 53% sequence similarity to porcine medium chain acyl-CoA dehydrogenase, and these similarities were utilized to predict structure-function relationships in glutaryl-CoA dehydrogenase.

L3 ANSWER 7 OF 14 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V. DUPLICATE 4

ACCESSION NUMBER: 91289002 EMBASE

DOCUMENT NUMBER: 1991289002

TITLE: Analysis of the polyadenylation consensus sequence context in the genes of nuclear encoded **mitochondrial proteins**.

AUTHOR: Juretic N.; Theus M.

CORPORATE SOURCE: Laboratorium fur Biochemie I, ETH Zentrum, CH-8092 Zurich, Switzerland

SOURCE: FEBS Letters, (1991) 290/1-2 (4-8).

ISSN: 0014-5793 CODEN: FEBLAL

COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 029 Clinical Biochemistry

LANGUAGE: English

SUMMARY LANGUAGE: English

AB A complication of the pre-mRNA ends of the genes of nuclear encoded mitochondrial resulted in a consensus sequence of the type (T/A)NTTNNNNNTTTNAATAAA. Nucleotide positions +8, +13, +16 and +17 downstream of the AATAAA sequence show also a predominance of nucleotide T. This consensus sequence suggests the importance of the immediate surroundings of the canonical polyadenylation signal sequence AATAAA on the efficiency of the cleavage and polyadenylation of this specific group of pre-mRNAs.

L3 ANSWER 8 OF 14 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1990:517606 BIOSIS

DOCUMENT NUMBER: BA90:134882

TITLE: ANTIBODIES AGAINST A FUSED GENE PRODUCT IDENTIFY THE PROTEIN ENCODED BY A GROUP II YEAST MITOCHONDRIAL INTRON.

AUTHOR(S): BERGANTINO E; CARIGNANI G

CORPORATE SOURCE: DIP. CHIM. BIOL. DELL'UNIV. PADOVA, I-VIA TRIESTE 75, 35121 PADOVA, ITALY.

SOURCE: MOL GEN GENET, (1990) 223 (2), 249-257.

CODEN: MGGEAE. ISSN: 0026-8925.

FILE SEGMENT: BA; OLD

LANGUAGE: English

AB In the mitochondrial genome of *Saccharomyces cerevisiae*, introns aI1 and

aI2 of the gene encoding the COX1 subunit are the only group II introns with open reading frames (ORFs); these can be translated into two homologous proteins, the maturase aI1 and aI2. These proteins are structurally related to viral reverse transcriptases and have been shown genetically to be involved in pre-mRNA splicing and in the deletion of introns from mitochondrial DNA. To identify these **mitochondrial proteins** and study their properties more directly, we raised antibodies against a part of the intron aI2 ORF translation product. For this purpose, we constructed series of fusion genes, by joining parts of the genes for protein A or lacZ to different portions of the intron aI2. These were expressed in Escherichia coli as hybrid polypeptides, which were used for the production and identification of specific antibodies against the yeast mitochondrial protein. The antibodies recognized the 57 kDa protein (maturase aI2) that accumulates in two yeast mutants deficient in the splicing of aI2. This protein corresponds to the translation product of the 3' part of intron aI2 and accumulates unaltered in the two cis-acting mutants.

L3 ANSWER 9 OF 14 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 5
 ACCESSION NUMBER: 1988:564612 CAPLUS
 DOCUMENT NUMBER: 109:164612
 TITLE: Mitochondrial biogenesis: recent developments and insights
 AUTHOR(S): Grivell, L. A.; Van der Veen, R.; Kwakman, J. H. J. M.; Oudshoorn, P.; Meijer, M.
 CORPORATE SOURCE: Lab. Biochem., Univ. Amsterdam, Amsterdam, 1098SM, Neth.
 SOURCE: Philosophical Transactions of the Royal Society of London, Series B: Biological Sciences (1988), 319(1193), 85-95
 CODEN: PTRBAE; ISSN: 0080-4622
 DOCUMENT TYPE: Journal; General Review
 LANGUAGE: English

AB Biosynthesis of a functional mitochondrion requires the coordinate expression of genes in both mitochondrial and nuclear DNAs. In yeast, 3 mitochondrial genes are split and **RNA splicing** plays a pivotal role in their expression. The recent finding that some introns are capable of self-splicing activity in vitro has permitted anal. of the mechanisms involved in RNA catalysis and may eventually shed light on the evolution of splicing mechanisms in general. Most **mitochondrial proteins** are encoded by nuclear genes, synthesized in the cytoplasm and imported by the organelle. The availability of cloned genes coding for several constituent subunits of the ubiquinol-cytochrome c reductase, which are imported by mitochondria, has allowed study of selected steps in the addressing of proteins to mitochondria and their intercompartmental sorting within the organelle. Recent developments are discussed.

L3 ANSWER 10 OF 14 LIFESCI COPYRIGHT 2003 CSA
 ACCESSION NUMBER: 88:82866 LIFESCI
 TITLE: Mitochondrial biogenesis: Recent developments and insights. MITOCHONDRIAL BIOGENESIS.
 AUTHOR: Grivell, L.A.; Van der Veen, R.; Kwakman, J.H.J.M.; Oudshoorn, P.; Meijer, M.; Leaver, C.J. [editor]; Lonsdale, D.M. [editor]
 CORPORATE SOURCE: Sect. Mol. Biol., Lab. Biochem. and Biotechnol. Cent., Univ. Amsterdam, Kruislaan 318, 1098SM Amsterdam, Netherlands
 SOURCE: PHILOS. TRANS. R. SOC. LOND., B., (1988) pp. 85-95. Meeting Info.: Meeting on Mitochondrial Biogenesis. London (UK). 28-29 May 1987.
 DOCUMENT TYPE: Book
 TREATMENT CODE: Conference; General Review
 FILE SEGMENT: K; G; N

LANGUAGE: English

SUMMARY LANGUAGE: English

AB Biosynthesis of a functional mitochondrion requires the coordinate expression of genes in both mitochondrial and nuclear DNAs. In yeast, three mitochondrial genes are split and **RNA splicing** plays a pivotal role in their expression. The recent finding that some introns are capable of self-splicing activity in vitro has permitted analysis of the mechanisms involved in RNA catalysis and may eventually shed light on the evolution of splicing mechanisms in general. Most **mitochondrial proteins** are encoded by nuclear genes, synthesized in the cytoplasm and imported by the organelle. Recent developments are discussed.

L3 ANSWER 11 OF 14 MEDLINE

ACCESSION NUMBER: 88096554 MEDLINE

DOCUMENT NUMBER: 88096554 PubMed ID: 2827115

TITLE: Genes of nuclear encoded **mitochondrial proteins**: evidence for a variant of the 3' splice-site consensus sequence.

AUTHOR: Juretic N; Jaussi R; Mattes U; Christen P

CORPORATE SOURCE: Biochemisches Institut, Universitat Zurich, Switzerland.

SOURCE: NUCLEIC ACIDS RESEARCH, (1987 Dec 23) 15 (24) 10083-6.
Journal code: 0411011. ISSN: 0305-1048.

PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 198802

ENTRY DATE: Entered STN: 19900305

Last Updated on STN: 19980206

Entered Medline: 19880223

AB The introns of animal nuclear genes and of viral genes encoding protein possess at their 3' splice-site the consensus sequence (CT)11NTCAG (Mount, S.M. (1982) Nucl. Acids Res. 10, 459-472; Green, M.R. (1986) Ann. Rev. Genet. 20, 671-708). However, the total 39 introns of the 5 imported **mitochondrial proteins** of higher eucaryotes whose gene structure has been determined to date show a predominance of 44% for base T at position -4. Apparently, a variant consensus sequence, i.e. (CT)11TTCAG, characterizes the genes of nuclear encoded **mitochondrial proteins**.

L3 ANSWER 12 OF 14 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE
6

ACCESSION NUMBER: 1987:380170 BIOSIS

DOCUMENT NUMBER: BA84:66667

TITLE: DEFICIENCY IN MESSENGER **RNA SPLICING** IN
A CYTOCHROME C MUTANT OF NEUROSPORA-CRASSA IMPORTANCE OF
CARBOXYL TERMINUS FOR IMPORT OF APOCYTOCHROME C INTO
MITOCHONDRIA.

AUTHOR(S): STUART R A; NEUPERT W; TROPSCHUG M

CORPORATE SOURCE: INST. PHYSIOL. CHEM. PHYS. BIOCHEM. ZELLBIOL., UNIV.
MUENCHEN, GOETHESTR. 33, 8000 MUENCHEN 2, FRG.

SOURCE: EMBO (EUR MOL BIOL ORGAN) J, (1987) 6 (7), 2131-2138.
CODEN: EMJODG. ISSN: 0261-4189.

FILE SEGMENT: BA; OLD

LANGUAGE: English

AB Molecular cloning and characterization of cytochrome c cDNA clones of Neurospora crassa wild-type (74A) and a cytochrome c-deficient mutant (cyc1-1) are described. Southern blot analysis of genomic DNA indicates that only one cytochrome c gene exists in the N. crassa genome. The cDNA sequence of the wild-type cytochrome c confirmed the previously determined protein sequence. Sequence analysis of the cyc1-1 cDNA for cytochrome c revealed the presence of a larger open reading frame, owing to the presence of an unspliced intron in the 3' end of the coding region.

Splicing of this intron is obviously prevented due to the presence of two base exchanges in the highly conserved intron consensus sequences. Consequently, *cyc1-1* synthesizes apocytochrome c with an altered carboxy terminus, 19 amino acids longer than the wild-type cytochrome c, with the final 27 amino acids being of an unrelated sequence. This alteration in the carboxy terminus renders the apocytochrome c incompetent for binding to mitochondria and, consequently, import into mitochondria. Thus, unlike other mitochondrial precursor proteins, where it has been demonstrated that the amino terminus alone is sufficient to target the protein to the mitochondria, an intact carboxy terminus is required for efficient import of apocytochrome c into mitochondria. This is independent confirmation for the view that the import pathway of cytochrome c is unique with respect to all other **mitochondrial proteins** studied to date.

L3 ANSWER 13 OF 14 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1985:369985 BIOSIS

DOCUMENT NUMBER: BA80:39977

TITLE: SELF-SPLICING OF YEAST MITOCHONDRIAL RIBOSOMAL AND MESSENGER RNA PRECURSORS.

AUTHOR(S): VAN DER HORST G; TABAK H F

CORPORATE SOURCE: SECTION MOLECULAR BIOLOGY, LAB. BIOCHEMISTRY, UNIV. AMSTERDAM, KRUISLAAN 318, 1098 SM AMSTERDAM, THE NETHERLANDS.

SOURCE: CELL, (1985) 40 (4), 759-766.

CODEN: CELLB5. ISSN: 0092-8674.

FILE SEGMENT: BA; OLD

LANGUAGE: English

AB Linear and circular splicing intermediates resembling intermediates that result from self-splicing of ribosomal precursor RNA of *Tetrahymena* are present in mitochondrial RNA. **Splicing** of yeast mitochondrial precursor RNA also occurs in vitro in the absence of **mitochondrial proteins**. The large rRNA gene, consisting of the intron and part of the flanking exon regions, was inserted behind the SP6 promoter in a recombinant plasmid and was transcribed in vitro. The resulting RNA shows self-catalyzed splicing via incorporation of GTP at the 5'-end of the excised intron, 5'- to 3'-exon ligation, and intron circularization. When purified mitochondrial RNA is incubated under similar conditions with α -³²P-GTP, the excised ribosomal intron RNA is also labeled, as well as several other RNA species. Some of these RNA are derived from excised introns from the multiply split gene coding for cytochrome subunit I.

L3 ANSWER 14 OF 14 MEDLINE

ACCESSION NUMBER: 82150212 MEDLINE

DOCUMENT NUMBER: 82150212 PubMed ID: 6278418

TITLE: Evidence for ribosomes involved in splicing of yeast mitochondrial transcripts.

AUTHOR: Schmelzer C; Schweyen R J

SOURCE: NUCLEIC ACIDS RESEARCH, (1982 Jan 22) 10 (2) 513-24. Journal code: 0411011. ISSN: 0305-1048.

PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 198205

ENTRY DATE: Entered STN: 19900317

Last Updated on STN: 19900317

Entered Medline: 19820527

AB We have investigated the processing of transcripts of the split gene COB in yeast mitochondrial DNA from cells whose mitochondrial translation was blocked by chloramphenicol for several generations of cell growth. First analysis of transcripts by electrophoresis and RNA/DNA-hybridization clearly showed that cell growth in the presence of CAP leads to an inhibition of processing yielding an increasing amount of splicing

intermediates of the COB transcript and decreasing amounts of the 18S mRNA coding for apocytochrome b. This observation is in accordance with the now widely favoured idea that **mitochondrial proteins** are involved in splicing of COB transcripts and that their reduction should hamper processing and - therefore - lead to an accumulation of pre-mRNAs. However, further information obtained by pulse-labeling of pre-mRNA in vivo in the presence of CAP for various times shows that even 30 minutes after addition of CAP a reduction of the processing rate is obtained. Based on these findings we conclude that maturation of mtRNAs is not only dependent on **mitochondrial proteins**, but also on a more direct interaction of the translation machinery and RNA processing whose nature is so far unknown.

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SEA MITOCHONDRIAL PROTEINS

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FILE 'CAPLUS, BIOSIS, MEDLINE, SCISEARCH, EMBASE, BIOTECHNO, TOXCENTER, ESBIODBASE, LIFESCI' ENTERED AT 07:49:30 ON 14 FEB 2003

L2 21 S L1 AND (SOLUTE CARRIER OR RNA SPLIC?)
L3 14 DUP REM L2 (7 DUPLICATES REMOVED)
L4 2 S L3 AND (CDNA OR CLONE)

=> d l4 ibib ab 1-2

L4 ANSWER 1 OF 2 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1987:380170 BIOSIS
DOCUMENT NUMBER: BA84:66667
TITLE: DEFICIENCY IN MESSENGER **RNA SPLICING** IN
A CYTOCHROME C MUTANT OF NEUROSPORA-CRASSA IMPORTANCE OF
CARBOXYL TERMINUS FOR IMPORT OF APOCYTOCHROME C INTO
MITOCHONDRIA.
AUTHOR(S): STUART R A; NEUPERT W; TROPSCHUG M
CORPORATE SOURCE: INST. PHYSIOL. CHEM. PHYS. BIOCHEM. ZELLBIOL., UNIV.
MUENCHEN, GOETHESTR. 33, 8000 MUENCHEN 2, FRG.
SOURCE: EMBO (EUR MOL BIOL ORGAN) J, (1987) 6 (7), 2131-2138.
CODEN: EMJODG. ISSN: 0261-4189.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB Molecular cloning and characterization of cytochrome c **cdna**
clones of Neurospora crassa wild-type (74A) and a cytochrome
c-deficient mutant (cycl-1) are described. Southern blot analysis of
genomic DNA indicates that only one cytochrome c gene exists in the N.
crassa genome. The **cdna** sequence of the wild-type cytochrome c
confirmed the previously determined protein sequence. Sequence analysis of
the cycl-1 **cdna** for cytochrome c revealed the presence of a
larger open reading frame, owing to the presence of an unspliced intron in
the 3' end of the coding region. Splicing of this intron is obviously
prevented due to the presence of two base exchanges in the highly
conserved intron consensus sequences. Consequently, cycl-1 synthesizes
apocytochrome c with an altered carboxy terminus, 19 amino acids longer
than the wild-type cytochrome c, with the final 27 amino acids being of an
unrelated sequence. This alteration in the carboxy terminus renders the
apocytochrome c incompetent for binding to mitochondria and, consequently,
import into mitochondria. Thus, unlike other mitochondrial precursor
proteins, where it has been demonstrated that the amino terminus alone is
sufficient to target the protein to the mitochondria, an intact carboxy
terminus is required for efficient import of apocytochrome c into
mitochondria. This is independent confirmation for the view that the
import pathway of cytochrome c is unique with respect to all other
mitochondrial proteins studied to date.

L4 ANSWER 2 OF 2 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 95271695 EMBASE
DOCUMENT NUMBER: 1995271695
TITLE: Cloning of glutaryl-CoA dehydrogenase **cdna**, and
expression of wild type and mutant enzymes in Escherichia
coli.
AUTHOR: Goodman S.I.; Kratz L.E.; DiGiulio K.A.; Biery B.J.;
Goodman K.E.; Isaya G.; Frerman F.
CORPORATE SOURCE: Department of Pediatrics, University Colorado School

Medicine, Denver, CO, United States
SOURCE: Human Molecular Genetics, (1995) 4/9 (1493-1498).
ISSN: 0964-6906 CODEN: HMGEE5
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We have cloned, sequenced, and expressed **cDNAs** encoding wild type human glutaryl-CoA dehydrogenase subunit, and have expressed a mutant enzyme found in a patient with glutaric acidemia type I. The mutant protein is expressed at the same level as the wild type in *Escherichia coli*, but has less than 1% of the activity of wild-type dehydrogenase. We also present evidence that the glutaryl-CoA dehydrogenase transcript is alternatively spliced in human fibroblasts and liver; the alternatively spliced mRNA, when expressed in *E. coli*, encodes a stable but inactive protein. Purified expressed human glutaryl-CoA dehydrogenase has kinetic constants similar to those of the previously purified porcine dehydrogenase. The primary translation product from in vitro transcribed glutaryl-CoA dehydrogenase mRNA is translocated into mitochondria and processed in the same manner as most other nuclear-encoded **mitochondrial proteins**. Human glutaryl-CoA dehydrogenase shows 53% sequence similarity to porcine medium chain acyl-CoA dehydrogenase, and these similarities were utilized to predict structure-function relationships in glutaryl-CoA dehydrogenase.

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